



SEQUENCE LISTING

<110> Willson, Tracy
Nicola, Nicos A.
Hilton, Douglas J.
Metcalf, Donald
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
ENCODING SAME

<130> Davies cc

<140> 09/051,843
<141> 1998-06-29

<160> 11

<170> PatentIn Ver. 2.0

<210> 1
<211> 1383
<212> DNA
<213> nuc. & predicted a.a. seq. of mNR4

<220>
<221> CDS
<222> (61)..(1338)

<220>
<221> unsure
<222> (121)
<223> n=authors are unsure of exact sequence in this
region

<220>
<221> unsure
<222> (122)
<223> n=authors are unsure of exact sequence in this
region

<220>
<221> unsure
<222> (123)
<223> n=authors are unsure of exact sequence in this
region

<220>
<221> unsure
<222> (640)
<223> n=authors are unsure of exact sequence in this
region

<220>
 <221> unsure
 <222> (641)
 <223> n=authors are unsure of exact sequence in this
 region

<220>
 <221> unsure
 <222> (642)
 <223> n=authors are unsure of exact sequence in this
 region

<400> 1
 tgaaaagata gaataaatgg cctcgtgccg aattcggcac gagccgaggc gagggcctgc 60

atg gcg cgg cca gcg ctg ctg ggc gag ctg ttg gtg ctg cta ctg tgg 108
 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1 5 10 15

acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 20 25 30

cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 35 40 45

tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 50 55 60

tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 85 90 95

gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 100 105 110

gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 130 135 140

tgg	ctc	cct	gga	agg	aat	aca	agc	cct	gac	aca	cac	tat	act	ctg	tac	540
Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	His	Tyr	Thr	Leu	Tyr	160
145					150					155						
tat	tgg	tac	agc	agc	ctg	gag	aaa	agt	cgt	caa	tgt	gaa	aac	atc	tat	588
Tyr	Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	175
				165					170							
aga	gaa	ggt	caa	cac	att	gct	tgt	tcc	ttt	aaa	ttg	act	aaa	gtg	gaa	636
Arg	Glu	Gly	Gln	His	Ile	Ala	Cys	Ser	Phe	Lys	Leu	Thr	Lys	Val	Glu	
			180					185					190			
cct	nnn	agt	ttt	gaa	cat	cag	aac	gtt	caa	ata	atg	gtc	aag	gat	aat	684
Pro	Xaa	Ser	Phe	Glu	His	Gln	Asn	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	
		195					200					205				
gct	ggg	aaa	att	agg	caa	tcc	tgc	aaa	ata	gtg	tct	tta	act	tcc	tat	732
Ala	Gly	Lys	Ile	Arg	Pro	Ser	Cys	Lys	Ile	Val	Ser	Leu	Thr	Ser	Tyr	
	210					215					220					
gtg	aaa	cct	gat	cct	cca	cat	att	aaa	cat	ctt	ctc	ctc	aaa	aat	ggg	780
Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	His	Leu	Leu	Leu	Lys	Asn	Gly	
	225				230					235					240	
gcc	tta	tta	gtg	cag	tgg	aag	aat	cca	caa	aat	ttt	aga	agc	aga	tgc	828
Ala	Leu	Leu	Val	Gln	Trp	Lys	Asn	Pro	Gln	Asn	Phe	Arg	Ser	Arg	Cys	
				245					250					255		
tta	act	tat	gaa	gtg	gag	gtc	aat	aat	act	caa	acc	gac	cga	cat	aat	876
Leu	Thr	Tyr	Glu	Val	Glu	Val	Asn	Asn	Thr	Gln	Thr	Asp	Arg	His	Asn	
			260					265					270			
att	tta	gag	gtt	gaa	gag	gac	aaa	tgc	cag	aat	tcc	gaa	tct	gat	aga	924
Ile	Leu	Glu	Val	Glu	Glu	Asp	Lys	Cys	Gln	Asn	Ser	Glu	Ser	Asp	Arg	
		275					280					285				
aac	atg	gag	ggt	aca	agt	tgt	ttc	caa	ctc	cct	ggg	gtt	ctt	gcc	gac	972
Asn	Met	Glu	Gly	Thr	Ser	Cys	Phe	Gln	Leu	Pro	Gly	Val	Leu	Ala	Asp	
	290					295					300					
gct	gtc	tac	aca	gtc	aga	gta	aga	gtc	aaa	aca	aac	aag	tta	tgc	ttt	1020
Ala	Val	Tyr	Thr	Val	Arg	Val	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Phe	
	305				310					315					320	
gat	gac	aac	aaa	ctg	tgg	agt	gat	tgg	agt	gaa	gca	cag	agt	ata	ggg	1068
Asp	Asp	Asn	Lys	Leu	Trp	Ser	Asp	Trp	Ser	Glu	Ala	Gln	Ser	Ile	Gly	
				325					330					335		
aag	gag	caa	aac	tcc	acc	ttc	tac	acc	acc	atg	tta	ctc	acc	att	cca	1116
Lys	Glu	Gln	Asn	Ser	Thr	Phe	Tyr	Thr	Thr	Met	Leu	Leu	Thr	Ile	Pro	
			340					345					350			

gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg 1164
 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 355 360 365
 ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt 1212
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380
 aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag 1260
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400
 tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg 1308
 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415
 ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc 1358
 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
 420 425
 tttcttgccct tcaatgtgac cctgt 1383

<210> 2
 <211> 426
 <212> PRT
 <213> nuc. & predicted a.a. seq. of mNR4

<220>
 <221> unsure
 <222> (21)
 <223> authors are unsure about the sequence assignment

<220>
 <221> unsure
 <222> (194)
 <223> authors are unsure about the sequence assignment

<400> 2
 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
 1 5 10 15
 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
 20 25 30
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
 35 40 45
 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
 50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80
 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
 85 90 95
 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
 100 105 110
 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125
 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
 130 135 140
 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
 145 150 155 160
 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
 165 170 175
 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
 180 185 190
 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
 195 200 205
 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
 210 215 220
 Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
 225 230 235 240
 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
 245 250 255
 Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
 260 265 270
 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
 275 280 285
 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
 290 295 300
 Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
 305 310 315 320
 Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
 325 330 335

Ser
 Glu
 con

Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
 340 345 350
 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
 355 360 365
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400
 Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
 405 410 415
 Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
 420 425

<210> 3
 <211> 1383
 <212> DNA
 <213> Human IL-13 receptor alpha-chain

<220>
 <221> CDS
 <222> (61)..(1338)

<400> 3
 gagtctaaca cggaccaagg agttttaacac gtcgcgccgg gttccgaggc gagaggctgc 60

atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc 108
 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15
 gcc gcc gcc ggg gcc ggg gcc ggg gcc ggc ggc cct acg gaa act cag cca 156
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 20 25 30
 cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204
 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
 35 40 45
 tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
 50 55 60
 tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300
 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65 70 75 80

act	cgt	cgt	tca	ata	gaa	gta	ccc	ctg	aat	gag	agg	att	tgt	ctg	caa	348
Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln	
				85					90					95		
gtg	ggg	tcc	cag	tgt	agc	acc	aat	gag	agt	gag	aag	cct	agc	att	ttg	396
Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu	
			100					105					110			
gtt	gaa	aaa	tgc	atc	tca	ccc	cca	gaa	ggt	gat	cct	gag	tct	gct	gtg	444
Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	
		115					120					125				
act	gag	ctt	caa	tgc	att	tgg	cac	aac	ctg	agc	tac	atg	aag	tgt	tct	492
Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser	
	130					135					140					
tgg	ctc	cct	gga	agg	aat	acc	agt	ccc	gac	act	aac	tat	act	ctc	tac	540
Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr	
	145				150					155					160	
tat	tgg	cac	aga	agc	ctg	gaa	aaa	att	cat	caa	tgt	gaa	aac	atc	ttt	588
Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe	
				165					170					175		
aga	gaa	ggc	caa	tac	ttt	ggt	tgt	tcc	ttt	gat	ctg	acc	aaa	gtg	aag	636
Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys	
			180				185						190			
gat	tcc	agt	ttt	gaa	caa	cac	agt	gtc	caa	ata	atg	gtc	aag	gat	aat	684
Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	
		195					200					205				
gca	gga	aaa	att	aaa	cca	tcc	ttc	aat	ata	gtg	cct	tta	act	tcc	cgt	732
Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg	
		210				215					220					
gtg	aaa	cct	gat	cct	cca	cat	att	aaa	aac	ctc	tcc	ttc	cac	aat	gat	780
Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn	Asp	
	225				230					235					240	
gac	cta	tat	gtg	caa	tgg	gag	aat	cca	cag	aat	ttt	att	agc	aga	tgc	828
Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	Cys	
				245					250					255		
cta	ttt	tat	gaa	gta	gaa	gtc	aat	aac	agc	caa	act	gag	aca	cat	aat	876
Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn	
			260					265					270			
gtt	ttc	tac	gtc	caa	gag	gct	aaa	tgt	gag	aat	cca	gaa	ttt	gag	aga	924
Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg	
		275					280					285				

aat	gtg	gag	aat	aca	tct	tgt	ttc	atg	gtc	cct	ggg	gtt	ctt	cct	gat	972
Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	
290						295					300					
act	ttg	aac	aca	gtc	aga	ata	aga	gtc	aaa	aca	aat	aag	tta	tgc	tat	1020
Thr	Leu	Asn	Thr	Val	Arg	Ile	Arg	Val	Lys	Thr	Asn	Lys	Leu	Cys	Tyr	
305					310					315					320	
gag	gat	gac	aaa	ctc	tgg	agt	aat	tgg	agc	caa	gaa	atg	agt	ata	ggg	1068
Glu	Asp	Asp	Lys	Leu	Trp	Ser	Asn	Trp	Ser	Gln	Glu	Met	Ser	Ile	Gly	
				325					330					335		
aag	aag	cgc	aat	tcc	aca	ctc	tac	ata	acc	atg	tta	ctc	att	gtt	cca	1116
Lys	Lys	Arg	Asn	Ser	Thr	Leu	Tyr	Ile	Thr	Met	Leu	Leu	Ile	Val	Pro	
			340					345					350			
gtc	atc	gtc	gca	ggg	gca	atc	ata	gta	ctc	ctg	ctt	tac	cta	aaa	agg	1164
Val	Ile	Val	Ala	Gly	Ala	Ile	Ile	Val	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	
		355					360					365				
ctc	aag	att	att	ata	ttc	cct	cca	att	cct	gat	cct	ggc	aag	att	ttt	1212
Leu	Lys	Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	
	370					375					380					
aaa	gaa	atg	ttt	gga	gac	cag	aat	gat	gat	act	ctg	cac	tgg	aag	aag	1260
Lys	Glu	Met	Phe	Gly	Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Lys	Lys	
385					390					395					400	
tac	gac	atc	tat	gag	aag	caa	acc	aag	gag	gaa	acc	gac	tct	gta	gtg	1308
Tyr	Asp	Ile	Tyr	Glu	Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	
				405					410					415		
ctg	ata	gaa	aac	ctg	aag	aaa	gcc	tct	cag	tgatggagat	aattttatttt					1358
Leu	Ile	Glu	Asn	Leu	Lys	Lys	Ala	Ser	Gln							
			420					425								
tac	ctt	cact	gtg	ac	ctt	ga	gaaga									1383

<210> 4
 <211> 426
 <212> PRT
 <213> Human IL-13 receptor alpha-chain

<400> 4
 Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
 1 5 10 15
 Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
 20 25 30

Pro	Val	Thr	Asn	Leu	Ser	Val	Ser	Val	Glu	Asn	Leu	Cys	Thr	Val	Ile
		35					40					45			
Trp	Thr	Trp	Asn	Pro	Pro	Glu	Gly	Ala	Ser	Ser	Asn	Cys	Ser	Leu	Trp
	50					55					60				
Tyr	Phe	Ser	His	Phe	Gly	Asp	Lys	Gln	Asp	Lys	Lys	Ile	Ala	Pro	Glu
	65				70					75					80
Thr	Arg	Arg	Ser	Ile	Glu	Val	Pro	Leu	Asn	Glu	Arg	Ile	Cys	Leu	Gln
				85					90					95	
Val	Gly	Ser	Gln	Cys	Ser	Thr	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Ile	Leu
			100					105					110		
Val	Glu	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val
		115					120					125			
Thr	Glu	Leu	Gln	Cys	Ile	Trp	His	Asn	Leu	Ser	Tyr	Met	Lys	Cys	Ser
	130					135					140				
Trp	Leu	Pro	Gly	Arg	Asn	Thr	Ser	Pro	Asp	Thr	Asn	Tyr	Thr	Leu	Tyr
	145				150					155					160
Tyr	Trp	His	Arg	Ser	Leu	Glu	Lys	Ile	His	Gln	Cys	Glu	Asn	Ile	Phe
				165					170					175	
Arg	Glu	Gly	Gln	Tyr	Phe	Gly	Cys	Ser	Phe	Asp	Leu	Thr	Lys	Val	Lys
			180					185					190		
Asp	Ser	Ser	Phe	Glu	Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn
		195					200					205			
Ala	Gly	Lys	Ile	Lys	Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	Arg
	210					215					220				
Val	Lys	Pro	Asp	Pro	Pro	His	Ile	Lys	Asn	Leu	Ser	Phe	His	Asn	Asp
	225				230					235					240
Asp	Leu	Tyr	Val	Gln	Trp	Glu	Asn	Pro	Gln	Asn	Phe	Ile	Ser	Arg	Cys
				245					250					255	
Leu	Phe	Tyr	Glu	Val	Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	His	Asn
			260					265					270		
Val	Phe	Tyr	Val	Gln	Glu	Ala	Lys	Cys	Glu	Asn	Pro	Glu	Phe	Glu	Arg
		275					280					285			
Asn	Val	Glu	Asn	Thr	Ser	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp
	290					295					300				

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
 305 310 315 320
 Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
 325 330 335
 Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
 340 345 350
 Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
 355 360 365
 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
 370 375 380
 Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
 385 390 395 400
 Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
 405 410 415
 Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
 420 425

<210> 5
 <211> 30
 <212> PRT
 <213> signal sequence of murine IL-3

<400> 5
 Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu Leu
 1 5 10 15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser
 20 25 30

<210> 6
 <211> 8
 <212> PRT
 <213> N-terminal FLAG epitope-tag

<400> 6
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 7
 <211> 31
 <212> DNA

<213> Oligo 1478 5'

<400> 7

agcttctaga acagaagttc agccacctgt g

31

<210> 8

<211> 30

<212> DNA

<213> Oligo 1480 5'

<400> 8

aactccacct tctacaccac ctgatctaga

30

<210> 9

<211> 5

<212> PRT

<213> NR4 Motif

<220>

<221> Unsure

<222> (3)

<223> Xaa may be any amino acid

<400> 9

Trp Ser Xaa Trp Ser
1 5

<210> 10

<211> 27

<212> PRT

<213> N-term amino acid sequence of mNR4 (major)

<220>

<221> Unsure

<222> (24)

<223> Xaa may be any amino acid

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25

<210> 11
<211> 27
<212> PRT
<213> N-term amino acid sequence of mNR4 (minor)

<220>
<221> Unsure
<222> (24)
<223> Xaa may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15
Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25